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PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of

Francois MALLET et al.

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For: METHOD FOR DETECTING THE EXPRESSION OF AN ENVELOPE PROTEIN OF
A HUMAN ENDOGENOUS RETROVIRUS AND USES OF A GENE CODING FOR
SAID PROTEIN

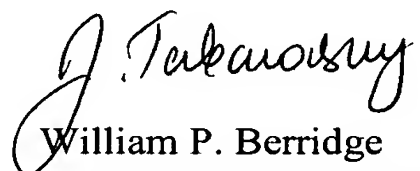
SUPPLEMENTAL RESPONSE TO SUPPLEMENTAL AMENDMENT

Commissioner for Patents
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Sir:

Further to the Supplemental Amendment filed October 26, 2007, Applicants submit
herewith, upon information and belief, an accurate English-language translation of French
Priority Application No. 99/11793 filed September 15, 1999.

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Retroviruses are enveloped viruses which bear glycoprotein spicules encoded by the viruses, at their surface. These envelope glycoproteins are synthesized in the form of polyprotein precursors (Pre-env) which are then cleaved by cellular proteases into mature surface (SU) protein and into transmembrane (TM) protein. Envelope glycoproteins are involved in the entry of viruses into host cells. They specifically recognize and bind to cell surface receptors and are necessary for the fusion of the viral envelope and the cell membranes of the host. The receptor and the envelope are multimeric or oligomeric molecules. For all enveloped viruses, the interactions of the envelope glycoproteins with the cellular receptor(s) lead to conformational rearrangements of the envelope required for exposure of the fusion peptide. The fusion takes place at the surface of the cell or in cellular vesicles, depending on the pathway of endocytosis of the virion. In addition, in order to allow entry of the virus, fusion mediated by the viral surface proteins may, under certain conditions, cause cell-to-cell fusion, resulting in the formation of giant multinucleated cells or syncytia. The formation of syncytia takes place via at least two pathways: a virion may simultaneously fuse with two cells, in which case reference is made to fusion "from without", or an infected cell which expresses the envelope glycoproteins at its surface may fuse with an adjacent cell (fusion "from within").

The envelope determinants and the sequence of events causing the conformational changes in the envelope during the processes of fusion "from without" are well documented for orthomyxoviruses which require an acid environment in the endocytosis vesicles in order to enter (Skehel, J.J. et al., PNAS, 79:968-972 (1982)). For retroviruses, for which the pathway of entry is independent of the pH, the precise

determinants and steps leading from the recognition of the receptor to the activation of the fusion have not yet been elucidated. Other retroviruses are known to induce cell-to-cell fusion ("fusion from within"), such as the feline leukemia virus, the mouse mammary tumor virus, the avian reticuloendotheliosis virus, HIV and SIV.

Moreover, Fefferery S. Jones and Rex Risser (Journal of Virology, Jan. 1993, p. 67-74) have shown that the envelope glycoproteins of the wild-type ecotropic murine leukemia virus (MuLV), under the control of the viral LTR, are capable of inducing the formation of syncytia in rat XC cells in the absence of virions (fusion "from within").

To the inventors' knowledge, the envelope glycoproteins of a human endogenous retrovirus have never been shown to have fusogenic power in a process of fusion "from within".

Some authors have indeed put forward the hypothesis that the endogenous retroviral envelope of ERV3, a human endogenous retrovirus close to MLV (Moloney leukemia virus), may be involved, *in vivo*, in the development of the placenta via a process of fusion (Patrick J.W. Venables et al., Virology, 211, 589-592 (1995)), but this phenomenon has never been demonstrated *in vitro*. Furthermore, studies on the polymorphism of ERV3 env on individuals of Caucasian origin, have made it possible to demonstrate the presence of a mutation in the (SU) region of the ERV3 envelope, generating an early stop codon present in the homozygous state in 1% of the population studied, without these individuals exhibiting any abnormality of pregnancy or of placental development (Nathalie de Parseval and Thierry Heidmann, Journal of Virology, Vol. 72, No. 4, pages 3442-3445 (1998)), this casting doubt over the hypothesis previously put forward.

The present inventors have now demonstrated, *in vitro*, that the unmodified HERV-W envelope glycoprotein, expressed under the control of a promoter, preferably a heterologous promoter, has fusogenic properties.

HERV-W is a recently described multicopy family of human endogenous retroviruses, so named because of the homology between the attachment site for the reverse transcription primer and that of avian retroviruses which use the Trp tRNA. No competent entity for its replication has been demonstrated. The functionality of a promoter region has been verified and, among various healthy human tissues tested, its expression appears, by Northern blot, to be restricted to the placenta (J.L. Blond et al., Journal of Virology, Vol. 73, No. 2, pages 1175-1185 (1999)). A single open reading frame coding for a potentially functional retroviral envelope exists on chromosome 7. A cDNA clone probably corresponding to a subgenomic transcript and bearing the complete sequence of the envelope has been isolated from placental material (clone cl.PH74, GenBank AF072506, the sequence of which is identified by SEQ ID No. 2). The phylogenetic studies carried out at the protein level indicate that the envelope protein is type D. The sequence SEQ ID No. 2 given at the end of the description therefore corresponds to the complete cDNA nucleotide sequence of the clone cl.PH74, the protein sequence of which is identified by SEQ ID No. 1.

Env HERV-W has all the "attributes" of a retroviral envelope: in particular, a leader peptide and the two characteristic subunits SU and TM separated by a furin cleavage site and, in its TM, it has a hydrophobic fusion peptide, an immunosuppressive region and a transmembrane carboxyl region followed by a long

cytoplasmic tail. Env HERV-W expression has been demonstrated in the placenta.

5 The experiments carried out by the inventors show that Env HERV-W causes, by cell-to-cell fusion, the formation of syncytia in various cell lines tested, of human and simian origin. The fusion phenomenon observed is dependent on the recognition of specific receptor(s), as shown directly in transfections and
10 indirectly in cocultures of transfected cells with other cell types. The present inventors have, moreover, identified the specific receptor for Env HERV-W using a competition approach based on the property of interference of retroviral envelopes, by blocking
15 cellular receptors with an envelope protein other than Env HERV-W, thus preventing the formation of syncytia. The receptor identified by the present inventors is the hATB^o receptor for type D mammalian retroviruses, which is expressed in human cells (Rasko E.J. et al. PNAS, 1999, 96: 2129-2134 and Tailor C.S. et al. J. Virol.,
20 1999, 73(5): 4470-4474). The use of this receptor, the method for the demonstration of which is described in one of the examples, is also part of the present invention.

25

Thus, a subject of the present invention is a method for detecting the expression of an envelope protein or polypeptide of a human endogenous retrovirus, according to which the protein or
30 polypeptide has a polypeptide sequence which comprises the sequence SEQ ID No. 1 or a fragment of SEQ ID No. 1, or a sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID
35 No. 1 or with a fragment of SEQ ID No. 1, and according to which the fusogenic power of said protein or of said fragment in cells of a cellular tissue or of a cell culture is detected by demonstrating the formation of syncytia.

Another subject of the invention is a method for detecting the expression of an envelope protein or polypeptide of a human endogenous retrovirus, according to which the protein or polypeptide has a polypeptide
5 sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID No. 1, and according to which the fusogenic power of said protein in cells of a cellular tissue or of a cell
10 culture is detected by demonstrating the formation of syncytia.

According to the invention, said protein or said polypeptide has a polypeptide sequence which comprises
15 the sequence SEQ ID No. 1 or a fragment of SEQ ID No. 1, or a sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID No. 1 or with a fragment of SEQ ID No. 1.
20

According to the present invention, it is clearly understood that said protein or said polypeptide, or said fragments thereof, if they do not exhibit complete identity with SEQ ID No. 1 or its fragments, should
25 have a fusogenic power preferably at least equal to or greater than that of SEQ ID No. 1 or its fragments.

If the fragments of the protein or of the polypeptide of the invention exhibit complete identity
30 with the fragments of SEQ ID No. 1, then the size of these fragments may be less than 20 amino acids, for example it may be approximately 10 amino acids, or even approximately 5 amino acids.

35 The variations envisaged according to the invention in the polypeptide sequence of the protein or of the polypeptide, or of their fragments, comprise the variations linked to the polymorphism, but also modifications such as substitution(s), deletion(s) and

addition(s) which may be introduced into said polypeptide sequence in order to obtain a protein, a polypeptide, or a fragment thereof, which has fusogenic power, in particular at least equal to or greater than
5 that of SEQ ID No. 1 or its fragments.

The polymorphism analysis may be carried out by the SSCP (single strand conformational polymorphism) method, which is an electrophoretic method which makes
10 it possible to objectify, using differences in migration, the presence of at least one mutation which distinguishes two short sequences (less than 250 bp). Thus, as illustrated in figure 4, after amplification on total DNA using the primers U6198 and L6186, or
15 U6189 and L6186, it is possible to analyze the polymorphism of the envelope located on chromosome 7 using the set of primers represented (U6302 to L6321), making it possible to generate a set of 10 overlapping fragments of suitable size. The polymorphism of one of
20 the subfragments may also be demonstrated by sequencing, mapping and/or restriction techniques, as appropriate, or more simply by a sandwich hybridization technique of the ELOSA type which makes it possible to distinguish as little as a point mutation (Cros P. et
25 al., European patent application EP 0 486 661).

Examples of polymorphic Env HERV-W sequences are represented in the attached figure 1, the corresponding DNA sequences being represented in figure 2. These
30 figures represent the alignment of protein and nucleic acid sequences obtained by sequencing clones derived from three different individuals.

Moreover, the polymorphism of the LTR which
35 directs the transcription of the env gene located on chromosome 7 was studied. Two groups of 5' LTRs are observed, the nucleic acid sequences of which, obtained by sequencing two clones originating from two different individuals, are represented and aligned in figure 3.

A judicious choice of primers has made it possible to specifically amplify, on chromosome 7, from total human DNA, a nucleic acid fragment containing all the information U3RU5-gag-pol-env-U3RU5, using the U6198 and L6186 primers, or exclusively the env-U3RU5 sequence, using the U6189 and L6186 primers. Such an approach is, for example, possible using a primer which overlaps the zone where the retrovirus sequence (U3 upstream, U5 downstream) joins the contiguous nonretroviral flanking sequence. For example, the L6186 primer overlaps the terminal 3' U5 region and the downstream nonretroviral sequence. Using such a PCR product isolating the sequence of interest from the mixture of HERV-W sequences present in the human genome, it is possible to carry out an analysis of the polymorphism.

Preferentially, said protein has at least one of the following characteristics:

- it is encoded by the env gene of the HERV-W endogenous retrovirus;
- it is encoded by an open reading frame located on chromosome 7 of the human genome;
- it has a polypeptide sequence which comprises the sequence SEQ ID No. 1, or a sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with SEQ ID No. 1. Preferably, it consists of SEQ ID No. 1.

The cells of said tissue or of said cell culture, in which demonstration of the fusogenic power is sought, are advantageously chosen from bone cells, muscle cells, placenta cells, endothelial cells, in particular of blood vessels, epithelial cells, glial cells and tumor cells or cells derived from tumor cell lines.

As will be illustrated in one of the following examples, the detection of the fusogenic power of said protein may be carried out according to at least any one of the following two protocols.

5

According to a first protocol, a vector for expression of said protein is obtained, based on which the expression of the protein or of its gene is under the control of a promoter, preferably a strong promoter; cells are transfected with the vector obtained, so as to obtain producer cells expressing, at their surface, said protein; and the formation of syncytia or the absence of formation of syncytia is observed.

15

According to a second protocol, a vector for expression of said protein is obtained, based on which the expression of the protein or of its gene is under the control of a promoter, preferably a strong promoter; cells are transfected with the vector obtained, so as to obtain producer cells expressing, at their surface, said protein; naïve indicator cells expressing, at their surface, a receptor for said protein are cocultured in the presence of said producer cells; and the formation of syncytia or the absence of formation of syncytia is observed.

25

The present invention also relates to the use of a gene or of a nucleic acid, or of a fragment of gene or of a nucleic acid, coding for a protein or a polypeptide as defined above in the description of the methods which are subjects of the invention, under suitable conditions which allow its expression, for preparing a therapeutic or prophylactic composition.

30

35

Another subject of the invention is a therapeutic or prophylactic composition comprising a gene or a nucleic acid, or a fragment of gene or of nucleic acid, coding for a protein or a polypeptide as defined above.

Such a composition may also comprise a heterologous or autologous promoter, preferably a heterologous promoter, for the expression of said
5 protein or of said polypeptide.

The invention also relates to the following subjects:

- 10 - an expression vector comprising at least one gene or one nucleic acid, or one fragment of gene or of nucleic acid, coding for a protein or a polypeptide as defined above, and elements required for its expression in a host cell;
- 15 - a host cell comprising at least one expression vector of the invention, and
- a therapeutic or prophylactic composition comprising at least one expression vector or one host cell of the invention.

20 The various therapeutic compositions of the invention are in particular intended for the treatment of cancers, such as by destroying the cancer cells by means of the formation of syncytia. The various prophylactic compositions of the invention are also
25 intended to prevent a deficiency in placental development or to prevent a deficiency in the natural formation of any other types of syncytia, said deficiency being associated with a pathology.

30 The therapeutic or prophylactic compositions of the invention, as defined above, are advantageously intended for a treatment commonly named "treatment by gene therapy" or "treatment by gene transfer".

35 As stated above, the fusogenic properties of the Env HERV-W protein, of the Env HERV-W polypeptide or of their fragments as defined in the present invention in particular find an application in the domain of cancer gene therapy.

To date, the genes most commonly used in therapy against cancers are (i) the genes which code for proteins which increase the immunogenicity of the tumor cells, such as pro-inflammatory cytokines, (ii) the genes which code for enzymes which make the cancer cells sensitive to a promedicament in gene/prodrug systems, such as the Herpes Simplex virus thymidine kinase/Ganciclovir system or the cytosine deaminase/5FC system.

Ideally, the transfer of therapeutic genes should lead both to a local destruction of the cancer cells and to activation of antitumor immunity in order to eliminate the tumor regions to which the therapeutic genes cannot be delivered, and the treatment should not cause damage to the host's normal cellular tissues, in particular to the tissues of the vital organs.

The protein or polypeptide of the invention, which comprises or consists of the Env HERV-W protein or its fragments, or of a polypeptide sequence which has, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with SEQ ID No. 1 or a fragment of SEQ ID No. 1, under the control of a heterologous or autologous promoter capable of inducing its expression, corresponds to the criteria defined above by the formation of syncytia. The syncytia form from one or more transfected cell(s) by a process of cell-to-cell fusion.

In an embodiment with a view to optimizing its therapeutic characteristics, the polypeptide of the invention, is optionally fused with one or more other protein(s) or protein fragment(s), even if intrinsically it corresponds to the criteria defined above. The polypeptide of the invention, or its fragment, is capable of inducing the formation of syncytia at a pH close to neutral or at neutral pH.

Typically, the expression vector or plasmid will be adjusted to allow expression of the polypeptide which induces the formation of syncytia, such that, when it is expressed, the polypeptide may induce the fusion of transfected cells with other nontransfected human cells. It is desirable for the protein or polypeptide of the invention to be expressed independently of other viral components, unless these components are useful for the vectorization.

10

Thus, a subject of the present invention is a gene or a nucleic acid, or a fragment of gene or of a nucleic acid, which is recombinant and which codes for a polypeptide of the invention which induces the formation of syncytia by fusion of transformed cells and target malignant cells, and its use in the domain of therapy for malignant diseases, such as cancers.

The invention also relates to a method for treating a malignant disease in a patient, which consists in administering to the patient the gene or a nucleic acid, or a fragment of gene or of a nucleic acid, which is recombinant and which codes for a protein, a polypeptide of the invention which induces the formation of syncytia by fusion of transformed cells and target malignant cells.

The gene or the nucleic acid, or the fragment of gene or of nucleic acid, is introduced *in vitro* into suitable human cells, such as cells of immortalized continuous lines, by standard techniques known to those skilled in the art, such as transfection, transduction or transformation, and the cells thus transformed are then introduced into the patient, where they may exert their fusogenic properties.

The gene or the nucleic acid, or the fragment of gene or of nucleic acid, of the invention may be used in various ways for the treatment of cancers, in

particular for the treatment of solid or soft tumors. The target cells may be transformed *ex vivo* or *in vivo* with the vectors (plasmids) coding for the polypeptide of the invention.

5

The fusogenic properties of the Env HERV-W protein, of the Env HERV-W polypeptide or of their fragments as defined in the present invention also find an application in the domain of prophylaxis, for preventing a deficiency in placental development and overcoming failed pregnancies.

The gene or the nucleic acid or their fragments as defined in the invention may therefore be used for various therapeutic or prophylactic effects, the ultimate aim being (i) to destroy the target cells by formation of syncytia inducing cell death in the target cells by a process of death other than cell death by apoptosis, or (ii) to induce or to promote the formation of syncytia, for example to overcome a deficiency in the formation of syncytiotrophoblasts during pregnancy, or to prevent a deficiency in the natural formation of any other type of syncytia, said deficiency being associated with a pathology.

25

The invention also relates to the use of the Env HERV-W protein, or of a fragment of Env HERV-W, as defined above, at the surface of a gene therapy vector comprising, *inter alia*, a gene, a nucleic acid sequence or an oligonucleotide of therapeutic interest capable of being expressed in a target cell or of hybridizing to a complementary nucleotide sequence from a target cell, said Env HERV-W protein or said fragment of this protein interacting with its cellular receptor described above, thus promoting the introduction of the gene, the nucleic acid sequence or the oligonucleotide of therapeutic interest into the target cell.

35

Thus, the invention relates to a gene therapy vector comprising an envelope protein or polypeptide of a human endogenous retrovirus, said protein or said polypeptide having a polypeptide sequence which
5 comprises the sequence SEQ ID No. 1 or a fragment of SEQ ID No. 1, or a sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID No. 1 or with a fragment of SEQ ID
10 No. 1. Preferably, the gene therapy vector of the invention comprises the sequence SEQ ID No. 1. In a particular embodiment of the invention, the gene therapy vector mentioned above consists of a conventional retroviral vector of the MLV type or of a
15 lentiviral vector pseudotype with all or part of the envelope protein of HERV-W as defined above, or alternatively of a synthetic vector carrying, at its surface, all or part of the Env HERV-W protein as defined above which confers the properties of cell
20 targeting and of plasma membrane fusion.

The invention also relates to a gene therapy vector comprising, at its surface, the receptor for the protein identified in SEQ ID No. 1, in particular for
25 targeting cells producing said protein in a constitutive or induced manner.

The nucleic acid sequences and/or oligonucleotides of therapeutic interest (antisense or coding for a
30 protein) in particular make it possible to target the cells in which a gene is expressed.

The antisense nucleic acid sequences or oligonucleotides are capable of interfering
35 specifically with the synthesis of a target protein, by inhibiting the formation and/or the functioning of the polysome, depending on the position of the antisense in the mRNA of the target. Therefore, the common choice of the sequence surrounding the translation initiation

codon as a target for inhibition by an antisense nucleic acid sequence or by an antisense oligonucleotide is aimed at preventing the formation of the initiation complex. Other mechanisms in the inhibition by antisense oligonucleotides involve activation of ribonuclease H, which digests the antisense oligonucleotide/mRNA hybrids, or interference at splicing sites by antisense oligonucleotides whose target is an mRNA splicing site. The antisense oligonucleotides are also complementary to DNA sequences and may therefore interfere at the level of transcription, by forming a triple helix, the antisense oligonucleotide pairing via "Hoogsteen" hydrogen bonds at the level of the major groove of the DNA double helix. In this particular case, reference is made more precisely to anti-gene oligonucleotides. It is clearly understood that the antisense nucleic acid sequences or oligonucleotides may be strictly complementary to the DNA or RNA target to which they must hybridize, but also not strictly complementary, on the condition that they hybridize on the target. Similarly, they may be antisense oligonucleotides which may or may not be modified at the level of the internucleotide bonds. All these notions are part of the general knowledge of those skilled in the art.

The present invention therefore relates to a therapeutic composition comprising, inter alia, a gene therapy vector, the Env HERV-W protein or a fragment of this protein as defined above, and an antisense nucleic acid sequence or oligonucleotide as defined above.

The Env HERV-W protein or one of its fragments is also used as a therapeutic vector for the transfer of a gene of therapeutic interest into a target cell and in the formulation of a therapeutic composition comprising at least one gene therapy vector, the Env HERV-W protein or a fragment of this protein as defined above, and a gene of therapeutic interest, and also the

elements which allow the expression of said gene of therapeutic interest. The genes of therapeutic interest may be nonmutated or mutated. They may also consist of nucleic acids modified such that it is impossible for
5 them to integrate into the genome of the target cell, or nucleic acids stabilized with agents, such as spermine.

The expression "elements which ensure the
10 expression of said gene of therapeutic interest *in vivo*" refers in particular to the elements required to ensure the expression of said therapeutic gene after it has been transferred into a target cell. They are, in particular, promoter sequences and/or regulatory
15 sequences which are effective in said cell and, optionally, the sequences required to allow the expression of a polypeptide at the surface of the target cells. The promoter used may be a viral, ubiquitous or tissue-specific promoter or a synthetic
20 promoter. By way of example, mention will be made of promoters such as the RSV (Rous Sarcoma Virus), MPSV, SV40 (Simian Virus), CMV (Cytomegalovirus) or vaccinia virus promoters. It is also possible to choose a promoter sequence specific for a given cell type or
25 activatable under defined conditions. The literature provides a great deal of information relating to such promoter sequences.

In another embodiment, use may be made, in a
30 therapeutic composition, of a cell expressing the Env HERV-W protein or a fragment of this protein as defined above, as a vehicle for one or more gene(s) which is large in size, due to the fusogenic properties of the protein or of its fragments, which allow the vector
35 cell to fuse with a host cell deficient for one or more given genes, thus making it possible to compensate for the deficient gene(s) (example: dystrophin).

The invention therefore also relates to such a cell and its use as a cellular vector.

5 The fusogenic properties or power of the protein
or of the polypeptide of the invention are also used in
a method for testing the effectiveness of and selecting
medicinal substances or drugs, or gene/prodrug systems,
capable of having a qualitative and/or quantitative
effect on their fusogenic power, by bringing said
10 medicinal substance or drug, or said gene/prodrug
system, into contact with cells of a cell culture
expressing said protein or said polypeptide, and
observing a regression in or a disappearance of the
formation of syncytia, it being understood that the
15 formation of syncytia in the natural state is
associated with a pathological condition. By way of
example, mention may be made of hemorrhagic phenomena,
the destruction or modification of neuronal cells, and
the exacerbated modification or destruction of
20 osteoblasts.

The invention also relates to a method for
selecting medicinal substances or drugs, or
gene/prodrug systems, capable of having a qualitative
25 and/or quantitative effect on the fusogenic power of a
protein or of a polypeptide as defined above. According
to this method, said medicinal substance or drug, or
said gene/prodrug system, is brought into contact with
cells of a cell culture expressing said protein or said
30 polypeptide, and a regression in or a disappearance of
the formation of syncytia is observed.

The invention also relates to the use of at least
one antisense nucleic acid sequence or of at least one
35 antisense oligonucleotide corresponding to the criteria
described above and capable of hybridizing and of
interfering specifically with the synthesis of the Env
HERV-W protein, and to a therapeutic composition
comprising, inter alia, said antisense nucleic acid

sequence or oligonucleotide, with the aim of obtaining, *in vivo*, a regression or a disappearance of syncytia associated with a pathological condition.

5 With the aim of obtaining, *in vivo*, regression of
the formation of syncytia or disappearance of syncytia
associated with a pathological condition, a therapeutic
composition is prepared which comprises, *inter alia*, a
ligand capable of recognizing the receptor identified
10 above and of inactivating or inhibiting the process of
formation of syncytia, said composition comprising at
least a ligand chosen from a monoclonal antibody, a
polyclonal antibody, a transmembrane antibody or a
fragment of said antibody or an inhibitor molecule,
15 said ligand being specific to the receptor of said
protein identified by SEQ ID NO:1, or a composition is
prepared which comprises a gene coding for a ligand
capable of being expressed, *in vivo*, in a target cell
or in a given target cell tissue, said gene being under
20 the control of the required elements which ensure its
expression after it has been transferred into the
target cell or cellular tissue.

 Thus, the term "ligand" is intended to mean any
25 molecule which is capable of recognizing said receptor
and/or of inhibiting its function. It may be, *inter*
alia, a monoclonal antibody or a polyclonal antibody,
or a monoclonal antibody or polyclonal antibody
fragment. It may also be a molecule which inhibits the
30 function of the receptor, the affinity constant of
which would be greater than that of the Env HERV-W
protein for its binding and attachment to the receptor.

 The production of polyclonal and monoclonal
35 antibodies is part of the general knowledge of those
skilled in the art. Mention may be made, by way of
reference, of Köhler G. and Milstein C. (1975):
Continuous culture of fused cells secreting antibody of
predefined specificity, *Nature* 256: 495-497 and

Galfre G. et al. (1977) Nature, 266: 522-550, for the production of monoclonal antibodies, and Roda A., Bolelli G.F.: Production of high-titer antibody to bile acids, Journal of Steroid Biochemistry, Vol. 13, pp 449-454 (1980), for the production of polyclonal antibodies. For the production of monoclonal antibodies, an immunogen may be coupled to Keyhole Limpet Hemocyanin (KLH peptide) as a support for the immunization, or to serum albumin (SA peptide). The animals are given an injection of immunogen using complete Freund's adjuvant. The sera and the hybridoma culture supernatants derived from the immunized animals are analyzed for their specificity and their selectivity, using conventional techniques, such as for example ELISA or Western blot assays. The hybridomas producing the most specific and the most sensitive antibodies are selected. Monoclonal antibodies may also be produced *in vitro* by cell culture of the hybridomas produced or by recovery of ascites fluid, after intraperitoneal injection of the hybridomas into mice. Whatever the method of production, by supernatant or by ascites, the antibodies are then purified. The purification methods used are essentially ion-exchange gel filtration and exclusion chromatography or immunoprecipitation. A number of antibodies sufficient to identify the most effective ones are screened in functional assays. The *in vitro* production of antibodies, of antibody fragments or of antibody derivatives, such as chimeric antibodies produced by genetic engineering, is well known to those skilled in the art.

More particularly, the term "antibody fragment" is intended to mean the F(ab)₂, Fab, Fab' or sFv fragments (Blazar et al., 1997, Journal of Immunology 159: 5821-5833 and Bird et al., 1988, Science 242: 423-426) of a native antibody, and the term "derivative" is intended, *inter alia*, to mean a chimeric derivative of a native antibody (see for example Arakawa et al., 1996, J.

Biochem 120: 657-662 and Chaudray et al., 1989, Nature 339: 394-397).

As mentioned above, gene therapy opens up the possibility of expressing such ligands *in vivo*, by administering therapeutic compositions comprising at least one gene coding for such a ligand. Such a gene of therapeutic interest codes, in particular, (i) either for at least one polyclonal or monoclonal antibody, or a monoclonal or polyclonal antibody fragment, or for a native transmembrane antibody, or a fragment of such an antibody, provided that the antibody or antibody fragment is expressed *in vivo* at the surface of a target cell or of target cells of a tissue and is capable of recognizing and of binding to said receptor, (ii) or for at least one inhibitory molecule as described above.

The expression "target cells" or "target cells of a tissue", as defined above, is intended to mean (i) either cells at the level of which the intention is to act so as to prevent or inhibit the formation of syncytia, (ii) or cells other than these but which are capable of expressing the ligand and, consequently, of inhibiting and/or blocking the functional activity of the receptor.

The expression "element which ensures the expression *in vivo* of said gene" refers in particular to the elements required to ensure its expression after it has been transferred into a target cell. They are, in particular, the promoter sequences and/or the regulatory sequences which are effective in said cell and, optionally, the sequences required to allow the expression, at their surface [sic], of an inhibitory polypeptide or molecule, as mentioned above. The promoter used may be a viral, ubiquitous or tissue-specific promoter or a synthetic promoter. Examples of such promoters have been described previously.

The term "transmembrane antibody" is intended to mean an antibody in which at least the functional region capable of recognizing and of attaching to the
5 receptor is expressed at the surface of the target cells so as to allow recognition and attachment. Such antibodies may consist of fusion polypeptides comprising an amino acid sequence defining the functional region and an amino acid sequence defining a
10 transmembrane polypeptide which allows the anchoring within the lipid bilayer of the membrane of the target cells or to the external surface of this lipid bilayer. Nucleic acid sequences coding for such transmembrane antibodies are described in the literature.

15

The expression "gene or nucleic acid sequence or their fragments" is intended to mean (i) an isolated native gene or nucleic acid or their isolated fragments obtained by enzymatic cleavage, or (ii) a gene or
20 nucleic acid or their fragments obtained by chemical synthesis using automatic synthesizers, such as the synthesizers marketed by Applied Biosystems.

The term "tumor cells" is intended to mean (i)
25 cells of immortalized cell lines or (ii) primary tumor cells removed from a patient.

The term "autologous promoter" is intended to mean a 5' LTR of HERV-W, on the condition that it is
30 functional, and the term "heterologous promoter" is intended to mean any promoter which does not belong to the HERV-W family, of viral, retroviral or cellular origin, optionally modified, on the condition that it is functional. Advantageously, the autologous or
35 heterologous promoter is a strong promoter, i.e. it is capable of inducing quantitatively significant expression of the protein or of the polypeptide.

The fusogenic power of Env HERV-W protein may also be used to promote the process of cell adhesion in the case of heterologous or homologous grafts or in cell repair processes.

5

Example 1:

Cell lines:

The TELCeB6 line (Cosset et al., Journal of Virology, 69 (12): 7430-7436 (1995)) derives from the
10 TELac2 line after transfection and clonal selection of an expression plasmid intended to produce Gag and Pol protein of the MoMLV (Moloney murine leukemia virus) type. The TELac2 line initially derives from human rhabdomyosarcoma cells TE671 (ATCC CRL 8805) and
15 expresses the nlsLacZ retroviral reporter vector (Takeuchi et al., Journal of Virology, 68 (12): 8001-8007 (1994)). The production of infectious retroviral particles by TELCeB6 cells depends on the envelope expression vectors transfected.

20

The cells are cultured in DMEM medium (Dulbecco modified Eagle medium - Life Technologies) with 10% of fetal calf serum (Life Technologies). In general, this medium was used for all the other cell types, i.e. the
25 TE671 (ATCC CRL 8805 - human rhabdomyosarcoma), A-431 (ATCC CRL-1555 - solid tumor, human epidermoid carcinoma), HeLa (ATCC CCL-2), COS (ATCC CRL-1651), PAE (pig aorta endothelial cells), XC (ATCC CCL-165 - rat sarcoma), NIH-3T3 and QTB (ATCC CRL-1708) cells.

30

Construction of the envelope expression vectors:

The pHCMV plasmid was used for the expression of env HERV-W. The FBASALF-ARless plasmid was used as a positive control for fusion; it produces a highly
35 fusogenic form of the amphotropic MLV envelope glycoprotein, modified by introducing a stop codon before the first amino acid of the intracytoplasmic peptide p2-R (Rein et al., Journal of Virology, 68 (3): 1773-1781 (1994)). env HERV-W cloned, in the antisense

direction, into the pHCMV plasmid was used as a negative control.

Transfection and cell-to-cell fusion tests
5 (coculture):

The envelope glycoprotein expression plasmids are transfected into the TELCeB6 cells by calcium phosphate precipitation (Cosset et al., Journal of Virology, 69 (10): 6314-6322 (1995)). The confluent TELCeB6 cells
10 expressing Env are fixed with 0.5% glutaraldehyde in PBS, 24 h after transfection. Staining with May-Grünwald and Giemsa solutions (MERCK) is then carried out according to the supplier's recommendations. It stains the nuclei violet and the cytoplasms mauve and
15 enables the syncytia to be visualized.

For the coculture experiments, the transfected cells are detached from the support, counted and then re-seeded at equal concentration (3×10^5 cell/well) in
20 6-well plates. Fresh indicator cells are then added to the transfected cells, at 10^6 per well, and the coculture is allowed to continue for 24 h. XGal (5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside) staining may then be carried out in order to stain the
25 nucleus of the TELCeB6 cells (Cosset et al., Journal of Virology, 69 (10): 6314-6322 (1995)). It is followed by staining with May-Grünwald and Giemsa solutions (MERCK), carried out according to the supplier's recommendations.

30

Most of the syncytia can be observed 18 to 24 hours after the beginning of transfection; the progressive detachment of the cells no longer allows observation or staining 36 hours after transfection.
35 The fusion observed corresponds to a fusion "from within", i.e. a cell-to-cell fusion, based on a cell expressing the envelope, as opposed to a fusion "from without" which corresponds to formation of syncytia subsequent to a virion-cell(s) fusion.

Table I below gives the results obtained regarding the capacity for cell-to-cell fusion of Env HERV-W by direct transfection, compared to that of the ARless control envelope. The TELCeB6 and TE671 cells correspond to lines of human origin. The COS cells are green monkey kidney cells. The XC cells are rat cells.

Table I

Envelope	fusion index ^a on			
	TELCeB6 cells	TE671 cells	COS cells	XC cells
Arless	33	8.6	inn.	40
HERV-W	61	24.7	36	0

^a The fusion index corresponds to the percentage $(N-S)/T$, in which N is the number of nuclei in syncytia, S is the number of syncytia and T is the total number of nuclei counted. inn. signifies innumerable, organized in a "network".

Table I shows that the results for Env HERV-W are at least as good as for the control on the cells of human origin. They are less good on the simian cells. Env HERV-W does not induce the formation of syncytia on rat cells.

Table II below gives the data observed in experiments of coculturing indicator cells with TELCeB6 cells transfected with pHCMV-env HERV-W. The type, origin and species of the indicator cells are indicated. The formation of syncytia is indicated by the term yes/no.

Table II

Species	Cell type	Origin	Fusion in coculture with TELCeB6
Human	TE671	Rhabdomyosarcoma	Yes
	A431	Epidermoid carcinoma	Yes
	HeLa	Epithelioid carcinoma	Yes
Monkey	COS	Fibroblast type	Yes
Pig	PAE	Endothelium	Yes
Rat	XC	Sarcoma	No
Mouse	3T3	Fibroblastic	Yes
Quail	QT6	Fibrosarcoma	No

Table II gives the results of the coculture experiments as a function of the cell lines tested. Syncytia are observed in human rhabdomyosarcoma (TE671), epidermoid carcinoma (A431) and epithelioid carcinoma (HeLa) cells, and also in monkey cells of the fibroblast type (COS), pig endothelium cells (PAE) and mouse cells of the fibroblast type (3T3). The fact that the human endogenous envelope Env HERV-W is capable of fusing in pig cells may pose problems in the context of organ transplantation (xenotransplantation).

Example 2:

Joint and then selective amplification of the LTR and of the envelope:

In order to study the polymorphism of the coding region of the envelope and of the associated 5' LTR U3 promoter region, located on chromosome 7, amplification specific for a 10 kb fragment is carried out using a pair of specific primers. In fact, given that the HERV-W family comprises many noncoding copies and in particular a considerable number of LTRs, this strategy makes it possible to specifically and jointly amplify the env region and its promoter sequence (5' LTR) located upstream, exclusively on chromosome 7. For this, use is made of a primer U6198 which hybridizes on a specific sequence located upstream of 5' LTR on

chromosome 7, and a primer L6186 which hybridizes in an overlapping manner on the 3' LTR U5 region and the adjacent cellular gene, on this same chromosome. Long distance PCR (or LD-PCR) is carried out under the following conditions, 1 × 5 min at 94°C, 10 × (10 sec at 94°C, 30 sec at 55°C, 8 min at 68°C), 25 × (10 sec at 94°C, 30 sec at 55°C, 8 min at 68°C + 10 sec/cycle), 1 × 7 min at 68°C, in the presence of amplification buffer (50 mM Tris HCL, pH 9.0, at 25°C, 15 mM (NH₄)₂SO₄, 0.1% Triton X-100); 1.5 mM MgCl₂, 0.25 mM of each dNTP, 330 nM of each primer (U6198 and L6186), 1U of DNA polymerase and also 200 ng of matrix (genomic DNA) in a final volume of 50 ml.

A nested "env" PCR and also a nested "LTR" PCR are carried out using this diluted 10 kb PCR product, in order to objectify the presence or absence of a polymorphism of these two regions. The dilution allows specific amplification from the LD-PCR product and not from the starting genomic material. The nested "env" PCR is carried out using the U6189 and L6186 primers, the U6189 [sic] primer being that used for the LD-PCR, the U6189 primer being located upstream of the env ATG. The 5' LTR U3 region is amplified with the U6460 and L5643 pair of primers. The U6460 primer hybridizes upstream of the 5' LTR, while the L5643 primer hybridizes in the R domain of the 5' LTR. The nested PCRs are carried out under the following conditions, 1 × 5 min at 94°C, 30 × (1 min at 94°C, 1 min at 53°C, 3 min at 72°C), 1 × 7 min at 72°C, in the presence of amplification buffer (10 mM Tris HCL, pH 8.3, 50 mM KCl), 1.5 mM MgCl₂, 0.25 mM of each dNTP, 330 nM of each primer, 1.25U of DNA polymerase and an aliquot of the LD-PCR amplification product, in a final volume of 50 ml.

Analysis of the polymorphism:

In order to objectify the presence or absence of a polymorphism, the nested PCR products can be analyzed

in various ways, in particular sequencing or analysis
by the SSCP (Single Strand Conformation Polymorphism)
technique which makes it possible to demonstrate the
presence of at least one mutation between two short
5 sequences with a mean size of 250 bp.

Polymorphism of the env gene: the use of 20
primers (10 even sense primers: 6302 to 6320, and 10
odd antisense primers: 6303 to 6321) makes it possible
10 to sequence the coding region of the envelope using the
nested envelope PCR product. These primers may also be
used for analysis of the polymorphism by SSCP. By way
of example, the sequences of the envelope genes of
three healthy donors labeled D6, D10 and D21, are
15 illustrated in figure 2. These sequences show the
existence of a low polymorphism rate. If the envelope
sequence of donor D6 is used as an arbitrary reference,
the sequence of the envelope of donor D21 has a
mutation at position 386 (T386C), the replacement of
20 the thymine with cytosine inducing an amino acid change
of valine to alanine (V128A by protein numbering).
Similarly, the sequence of the envelope gene of donor
D10 has two mutations relative to the sequence of donor
D6, at position 671 (T671C) and 920 (G920A), inducing
25 two amino acid changes, from valine to alanine (V224A
by protein numbering) and from serine to asparagine
(S306N by protein numbering), respectively. These
sequences illustrate the existence of a polymorphism.
12 patient DNAs were sequenced, which made it possible
30 to observe a low polymorphism rate between the DNAs
tested. For example, comparison of the sequences
derived from two individuals, noted 10 and 21, shows
the presence of a nucleic acid difference of three
bases over the 1617 bases of the gene, which
35 corresponds to a polymorphism rate of 0.19%. Two
mutations are located on the sequence of DNA 10 (T671C
and G920A) and one on the sequence of DNA 21 (T386C).
The sequence of individual 6 is used as the reference.
This same analysis at the protein level makes it

possible to observe 3 mutated amino acids for the entire envelope comprising, in total, 538 amino acids, i.e. a polymorphism rate of 0.56%. The two mutations of the sequence derived from individual 10 are V224A and
5 S306N, and that of the sequence derived from individual 21 is V128A.

Polymorphism of the LTR5' U3 promoter region associated with the envelope gene: the sequencing of
10 the 5' LTR U3 domain is carried out using the 2 primers previously used for the nested LTR PCR. By way of example, the sequences of the 5' LTR U3 region (associated with the envelope gene) of two of the healthy donors (labeled D6 and D21), for which the
15 envelope has, moreover, been sequenced, are illustrated in figure 3. These sequences show the existence of a polymorphism rate which is higher than for the envelope gene. The variations at positions 210 (T for D6, C for D21), 211 (G for D6, A for D21), 229 (A for D6, G for
20 D21), 231 (T for D6, C for D21) and 232 (C for D6, A for D21) will in particular be noted.

The sequences of the primers used for the PCR, the SSCP and the sequencing are illustrated in table III
25 below.

Table III

NAME :	NUCLEOTIDE SEQUENCES :
	Long distance PCR primers
U6198 :	5'- CAA-AAC-GCC-TGG-AGA-TAC-AGC-AAT-TAT-C-3'
L6186 :	5'- GCA-CCC-TCA-TGG-TTG-TGT-TAC-TTG-G-3'
	Nested env PCR primers
U6189 :	5'- CTG-AAA-ATC-CAG-GAG-ACA-ACG-CTA-GC-3'
L6186 :	5'- GCA-CCC-TCA-TGG-TTG-TGT-TAC-TTG-G-3'
	Nested 5' LTR PCR primers
U6460 :	5'- TTG-GTA-CCC-AAA-ACG-CCT-GGA-GAT-ACA-GCA-ATT-ATC-3'
L5643 :	5'- AAC-TCG-AGT-GAA-ATA-GCA-TGA-AAA-CAG-AG-3'
	SSCP and env sequencing primers
U6302 :	5'- AGG-AAA-GTA-ACT-AAA-ATC-ATA-AAT-C-3'
L6303 :	5'- GGT-TCC-CTT-AGA-AAG-ACT-CC-3'
U6304 :	5'- AAT-ATT-GAT-GCC-CCA-TCG-TAT-A-3'
L6305 :	5'- CCA-GTT-TGG-GTG-AAG-TAA-GTC-3'

U6306 :	5'- GGA-GGA-CTT-GGA-GTC-ACT-GTC-3'
L6307 :	5'- AGG-CGA-GTA-TGG-GTA-CGG-AG-3'
U6308 :	5'- GGA-CTA-GAT-CTC-TCA-AAA-CTA-CA-3'
L6309 :	5'- ACG-GAA-GTG-GTG-TTT-ATT-TCT-G-3'
U6310 :	5'- CCT-GAA-CAA-TGG-AAC-AAC-TTC-3'
L6311 :	5'- ATT-CCT-GAG-GGT-AGG-CAG-AC-3'
U6312 :	5'- GGT-AAC-TCC-TCC-CAC-ACA-AA-3'
L6313 :	5'- GAA-TGG-GTA-CTC-TTT-TGT-TGC-3'
U6314 :	5'- TAC-AGT-TAT-GTC-ATA-TCT-AAG-CC-3'
L6315 :	5'- TAA-GTT-GAT-CTT-GCA-AGG-TGA-C-3'
U6316 :	5'- CTA-AAT-GGG-GAC-ATG-GAA-CG-3'
L6317 :	5'- TAT-TCG-ATC-TGG-AAT-TTC-TTC-AAC-3'
U6318 :	5'- CAA-TCC-GGA-ATC-GTC-ACT-GA-3'
L6319 :	5'- AGA-CAA-AGT-TAA-CAA-GGA-GGT-TC-3'
U6320 :	5'- ACT-CCT-CTT-TGG-ACC-CTG-TAT-C-3'
L6321 :	5'- GAG-GTT-GGC-CGA-CCA-CCG-3'

U refers to sense primers and L refers to reverse primers.

5

Example 3:

Interference tests were carried out in order to determine the receptor recognized by the envelope glycoprotein of HERV-W among the receptors known to be expressed in human cells, i.e. PiT-2 (the receptor for amphotropic MLVs), PiT-1 (the receptor for GALV - gibbon ape leukemia virus and FeLV-B - feline leukemia virus type B) and hATB^o (the receptor for type D mammalian retroviruses, also recognized by the RD114 retrovirus). For this, TELCeB6 cells were transfected either with the expression plasmid coding for the HERV-W envelope, with the expression plasmid expressing the antisense messenger RNA for the gene coding for the HERV-W envelope, or with the expression plasmid coding for a hyperfusogenic variant of the amphotropic MLV envelope named ARless. These cells, named "producer cells", were then cocultured with human cells, termed "indicator cells", expressing the receptor for the

10

15

20

HERV-W envelope, and which also stably expressed either the envelope of GALV, the envelope of amphotropic MLV, or the envelope of RD114. The expression of these diverse envelope glycoproteins on these cells is capable of recognizing the corresponding receptors, of blocking them and therefore of decreasing their ability to interact with a retroviral envelope glycoprotein corresponding to them but expressed exogenously at the surface of the "producer" cells. Thus, if during the tests for fusion by coculturing a decrease is observed in the formation of syncytia for an indicator cell type which blocks one of these receptors compared to the parental indicator cell for which all of the three potential receptors are fully accessible, the nature of the receptor recognized by the envelope expressed on the producer cell may be deduced therefrom. After coculturing for two days, the cells are fixed and stained and the fusion indices determined. The results are given in table IV below.

Table IV

Envelope protein expressed in the producer cells	Envelope proteins expressed in the indicator cells			
	Control	MLV-A	GALV	RD114
Arless	+	-	+	+
HERV-W antisense	-	-	-	-
HERV-W	+	+	+	-

- signifies a lack of syncytia and + signifies the presence of syncytia

Control signifies that there is no envelope protein expressed in this cell.

These results make it possible to deduce that the envelope glycoprotein of HERV-W recognizes the hATB^o receptor for type D mammalian retroviruses. Specifically, although this envelope is fusogenic for the parental indicator cells or for the indicator cells expressing either the MLV-A envelope or the GALV

envelope, no syncytia are observed when the producer cells expressing the envelope glycoprotein of HERV-W are cocultured with the indicator cells expressing the RD114 envelope.

CLAIMS

1. A method for detecting the expression of an envelope protein or polypeptide of a human endogenous retrovirus, characterized in that the protein or polypeptide has a polypeptide sequence which comprises the sequence SEQ ID No. 1 or a fragment of SEQ ID No. 1, or a sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID No. 1 or with a fragment of SEQ ID No. 1, and in that the fusogenic power of said protein or of said fragment in cells of a cellular tissue or of a cell culture is detected by demonstrating the formation of syncytia.
2. A method for detecting the expression of an envelope protein or polypeptide of a human endogenous retrovirus, characterized in that the protein or polypeptide has a polypeptide sequence which exhibits, for any series of 20 amino acids, at least 80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID No. 1, and in that the fusogenic power of said protein in cells of a cellular tissue or of a cell culture is detected by demonstrating the formation of syncytia.
3. The method as claimed in claim 1 or 2, characterized in that the protein is encoded by the env gene of the HERV-W endogenous retrovirus.
4. The method as claimed in claim 3, characterized in that the protein is encoded by an open reading frame located on chromosome 7 of the human genome.
5. The method as claimed in claim 4, characterized in that the protein has a polypeptide sequence which exhibits, for any series of 20 amino acids, at least

80%, preferably at least 90%, or even at least 95% identity with the sequence SEQ ID No. 1.

5 6. The method as claimed in claim 5, characterized in that the protein has a polypeptide sequence which consists of SEQ ID No. 1.

10 7. The method as claimed in any one of the preceding claims, characterized in that the cells of said tissue or of said cell culture are chosen from bone cells, muscle cells, placenta cells, endothelial cells, in particular of blood vessels, epithelial cells, glial cells and tumor cells or cells derived from tumor cell lines.

15 8. The method as claimed in any one of the preceding claims, characterized in that the detection of the fusogenic power of said protein consists in:
obtaining a vector for expression of said protein,
20 based on which the expression of the protein or of its gene is under the control of a promoter, preferably a strong promoter,
transfecting cells with the vector obtained, so as to obtain producer cells expressing, at their surface,
25 said protein, and
observing the formation of syncytia or the absence of formation of syncytia.

30 9. The method as claimed in any one of the preceding claims, characterized in that the detection of the fusogenic power of the protein consists in:
obtaining a vector for expression of said protein,
based on which the expression of the protein or of its gene is under the control of a promoter, preferably a
35 strong promoter,
transfecting cells with the vector obtained, so as to obtain producer cells expressing, at their surface, said protein,

coculturing naïve indicator cells, expressing, at their surface, a receptor for said protein, in the presence of said producer cells, and
5 observing the formation of syncytia or the absence of formation of syncytia.

10. The use of a gene or of a nucleic acid, or of a fragment of gene or of a nucleic acid, coding for a protein or a polypeptide as defined in any one of
10 claims 1, 6 or 9, under suitable conditions which allow its expression, for preparing a therapeutic or prophylactic composition.

11. The use as claimed in claim 10, characterized in
15 that said composition is intended for the treatment of cancers.

12. The use as claimed in claim 10, characterized in that said composition is intended to prevent a
20 deficiency in placental development or to prevent a deficiency in the natural formation of any other type of syncytia, said deficiency being associated with a pathology.

25 13. The use as claimed in claim 10, 11 or 12, characterized in that the composition is intended for treatment by gene therapy.

14. A therapeutic or prophylactic composition
30 comprising a gene or a nucleic acid, or a fragment of gene or of nucleic acid, coding for a protein or a polypeptide as defined in any one of claims 1 to 6.

15. The composition as claimed in claim 14,
35 characterized in that it also comprises a heterologous or autologous promoter, preferably a heterologous promoter, for the expression of said protein or of said polypeptide.

16. An expression vector comprising at least one gene or one nucleic acid, or one fragment of gene or of nucleic acid, coding for a protein or a polypeptide as
5 defined in any one of claims 1 to 6, and elements required for its expression in a host cell.

17. A host cell comprising at least one vector as claimed in claim 16.

10

18. A therapeutic or prophylactic composition comprising at least one expression vector as claimed in claim 16.

15 19. The use of a composition as claimed in any one of claims 14, 15 and 18, characterized in that said composition is intended for the treatment of cancers by destroying cancer cells by means of the formation of syncytia.

20

20. The use of a composition as claimed in any one of claims 14, 15 and 18, characterized in that said composition is intended to prevent a deficiency in placental development or to prevent a deficiency in the
25 natural formation of any other type of syncytia, said deficiency being associated with a pathology.

21. The use of a protein or of a polypeptide as defined in any one of claims 1 to 6, in a gene therapy
30 vector, said gene therapy vector comprising, inter alia, a protein or a polypeptide as defined in any one of claims 1 to 6.

22. A gene therapy vector comprising a protein or a
35 polypeptide as defined in any one of claims 1 to 6.

26. A vector as claimed in claim 22, chosen from a retroviral vector of the MLV type, a lentiviral vector

pseudotyped with a protein or a polypeptide as defined in any one of claims 1 to 6, and a synthetic vector.

24. A therapeutic composition comprising, inter alia,
5 a therapy vector as defined in either of claims 22 and 23, and an antisense nucleic acid sequence or oligonucleotide.

25. A therapeutic composition comprising, inter alia,
10 a therapy vector as defined in either of claims 22 and 23, and a gene of therapeutic interest.

26. A cell expressing a protein or a polypeptide as defined in any one of claims 1 to 6.

15 27. The use of a cell as claimed in claim 26, as a cellular vector.

28. A therapeutic composition comprising, inter alia, a cell or a cellular vector as defined in claims 26 and
20 27.

29. A method for selecting medicinal substances or drugs, or gene/prodrug systems, capable of having a qualitative and/or quantitative effect on the fusogenic
25 power of a protein or of a polypeptide as defined in any one of claims 1 to 6, according to which said medicinal substance or drug, or said gene/prodrug system, is brought into contact with cells of a cell culture expressing said protein or said polypeptide,
30 and a regression or a disappearance of the formation of syncytia is observed.

30. A therapeutic composition comprising, inter alia, an antisense nucleic acid sequence or oligonucleotide
35 capable of hybridizing to a gene or a fragment of gene, or to a nucleic acid or fragment of nucleic acid, coding for a protein or a polypeptide as defined in any one of claims 1 to 6.

31. A therapeutic composition comprising, inter alia, a ligand capable of recognizing and binding to the receptor for the protein defined in SEQ ID No. 1.

5

32. The therapeutic composition as claimed in claim 31, comprising at least one ligand chosen from a monoclonal antibody, a polyclonal antibody, a transmembrane antibody or a fragment of said
10 antibodies, and an inhibitory molecule, said ligand being specific for the receptor of the protein defined in SEQ ID No. 1.

33. A therapeutic composition comprising, inter alia,
15 a gene of therapeutic interest, said gene coding for a ligand as defined in claim 32 and being placed under the control of the elements required to ensure its expression *in vivo*.

20 34. A gene therapy vector comprising, at its surface, the receptor for the protein identified in SEQ ID No. 1, in particular to target cells producing said protein in a constitutive or induced manner.



LISTE DE SEQUENCES

<110> BIO MERIEUX

5 <120> Procédé de détection de l'expression d'une protéine
d'enveloppe d'un rétrovirus endogène humain et
utilisations d'un gène codant pour cette protéine

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<130> Pouvoir fusogène de env de ERV-W

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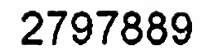
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25	atccaggaga caacgctagc tattcctgtg aacctctaga ggatttgccc ctgctcttca 720		
	aacaacaacc aggaggaaa taactaaaat cataaatccc catggccctc ccttatcata 780		
	tttttctctt tactgttctt ttaccctctt tcaactctac tgcacccctc ccatgcccgt 840		
	gtatgaccag tagctcccct taccaagagt ttctatggag aatgcagcgt cccggaaata 900		
	ttgatgcccc atcgtatagg agtctttcta agggaacccc caccttcact gccacacccc 960		
30	atatgccccg caactgctat cactctgcca ctctttgcat gcatgcaaat actcattatt 1020		
	ggacaggaaa aatgattaat cctagtgtgc ctggaggact tggagtcaact gtctgttgga 1080		
	cttacttcac ccaaactggg atgtctgatg ggggtggagt tcaagatcag gcaagagaaa 1140		
	aacatgtaaa agaagtaatc tcccaactca cccgggtaca tggcacctct agcccctaca 1200		
	aaggactaga tctctcaaaa ctacatgaaa ccctccgtac ccatactcgc ctggtaagcc 1260		
35	tatttaatac caccctcact gggctccatg aggtctcggc ccaaaaccct actaactggt 1320		
	ggatatgect cccctgaac ttcaggccat atgtttcaat ccctgtacct gaacaatgga 1380		
	acaacttcag cacagaaata aacaccactt ccgttttagt aggacctctt gtttccaatc 1440		
	tggaaataac ccatacctca aacctcacct gtgtaaaatt tagcaatact acatacacia 1500		
	ccaactccca atgcatcagg tgggtaactc ctccacaca aatagtctgc ctaccctcag 1560		
40	gaatattttt tgtctgtggt acctcagcct atcgttgttt gaatggctct tcagaatcta 1620		

tgtgcttccct ctcattctta gtgcccccta tgaccatcta cactgaacaa gatttatata 1680
 gttatgtcat atctaagccc cgcaacaaaa gagtaccat tcttcctttt gttataggag 1740
 cgggagtgcct aggtgcacta ggtactggca ttggcgggtat cacaacctct actcagttct 1800
 actacaaact atctcaagaa ctaaattggg acatggaacg ggtcgccgac tccctggtca 1860
 5 ccttgcaaga tcagcttaac tccctagcag cagtagtcct tcaaaatcga agagcttttag 1920
 acttgctaac cgctgaaaga gggggaacct gtttattttt aggggaagaa tgctgttatt 1980
 atgttaatca atccggaatc gtcactgaga aagttaaaga aattcgagat cgaatacaac 2040
 gtagagcaga ggagcttcga aacactggac cctggggcct cctcagccaa tggatgccct 2100
 ggattctccc cttcttagga cctctagcag ctataatatt gctactcctc tttggaccct 2160
 10 gtatctttaa cctccttggt aactttgtct cttccagaat cgaagctgta aaactacaaa 2220
 tggagcccaa gatgcagtc aagactaaga tctaccgcag acccctggac cggcctgcta 2280
 gcccacgac tgatgttaat gacatcaaag gcacccctcc tgaggaaatc tcagctgcac 2340
 aacctctact acgcccacat tcagcaggaa gcagttagag cggtcgtcgg ccaacctccc 2400
 caacagcact taggttttcc tgttgagatg ggggactgag agacaggact agctggattt 2460
 15 cctaggctga ctaagaatcc ctaagcctag ctgggaaggt gaccacatcc acctttaaac 2520
 acggggcctg caacttagct cacacctgac caatcagaga gctcactaaa atgctaatta 2580
 ggcaaagaca ggaggtaaag aaatagccaa tcctctattg cctgagagca cagcaggagg 2640
 gacaatgatc gggatataaa cccaagtctt cgagccggca acggcaaccc cctttgggtc 2700
 cctcccttt gtatgggagc tctgttttca tgctatttca ctctattaaa tcttgcaact 2760
 20 gcaaaaaaaaa aaaaaaaaaa a 2781

FIG. 2



Consensus	ATGCGCTCC	CTATCATAT	TTATCTCTT	ACTGTCTTT	TAAGCTCTT	CACTCTACT	GAAGCGCTC	CAATGCGCTG	TATGACGCTT	AGCTCGCTT	ACCAAGACTT	TCTATCGAGA	120
Env ADN 6	120
Env ADN 10	120
Env ADN 21	120
Consensus	ATGCGCTC	CCGAAATAT	TAATGCCCA	GTCTTCTTA	GGAAGCCCG	ACCTTCACTG	CCACACCCA	TATGCCCGC	AACTGCTATC	ACTCTGCCAC	TCTTTGCCATG	240	
Env ADN 6	240	
Env ADN 10	240	
Env ADN 21	240	
Consensus	CATGCAATA	CTCATATATG	GACAGGAAA	ATGATTAATC	CTAGTGTCC	TGAGGACTT	GGAATCACTG	TCTTTTGAC	TTACTTCAAC	CAAACTGTA	TGTCTGATCG	GCGTGAGTT	360
Env ADN 6	360
Env ADN 10	360
Env ADN 21	360
Consensus	CAGATGCG	CAGAGAAA	ACATGAAAA	CAATATATC	CCCAACTAC	CCGGTACTC	GCAACTCTA	GGCCTACAA	AGGACTAGAT	CTCTAAATAC	TACTGAAAC	CCCTCGTACC	480
Env ADN 6	480
Env ADN 10	480
Env ADN 21	480
Consensus	CATCTGCG	TGTAAGCCT	ATTATATAC	ACCTCTACTG	GCTCTACGA	GATCTGCGC	CAAAACCTTA	CTAACTCTTG	GATATGCTC	CCCTGAACT	TGAGGCAATA	TGTTTCAATC	600
Env ADN 6	600
Env ADN 10	600
Env ADN 21	600
Consensus	CTGTACTG	AACATGAAA	CAACTGCG	ACAGAAATA	ACAGCTCTC	CGTTTATGA	GCACTCTTG	TTCTCAATCT	GGAAATAC	CAATGCTCA	ACTCTACCTG	TGTAAATATT	720
Env ADN 6	720
Env ADN 10	720
Env ADN 21	720
Consensus	AGCATACTA	CATACACAC	CACTGCCA	TGCAATGAT	GCGTACTCC	TGCAACAAA	ATAGTCTCC	TACCTCTCG	AAATTTTTT	GTCTGTGTA	CCTCAGCTTA	TGCTGTGTTG	840
Env ADN 6	840
Env ADN 10	840
Env ADN 21	840
Consensus	ATGCGCTCT	CAGATCTAT	GTCTCTCTC	TGATCTTAG	TGCGCCCTAT	GAACATCAC	ACTGACACAG	ATTATACAT	TATGTCTATA	TCTAAGCCG	GCACAAAG	ACTACCCATT	960
Env ADN 6	960
Env ADN 10	960
Env ADN 21	960
Consensus	CTTCTCTTG	TTATAGGAC	AGCACTCTA	GATGCACTAG	GTACTGCCAT	TGGCGTATC	ACAACCTTA	CTCACTCTA	CTACAACTA	TCTCAGAAC	TAAATGGGA	CATGAAACGG	1080
Env ADN 6	1080
Env ADN 10	1080
Env ADN 21	1080
Consensus	GTCCCGACT	CCCTGCTAC	CTTGCAGAT	CAACTTACT	CCCTAGACG	AGTATGCTTT	CAAAATGAA	GAGCTTTAGA	CTTGTCAAC	GCTGAAAGG	GGCGAACCTG	TTTATTTTTA	1200
Env ADN 6	1200
Env ADN 10	1200
Env ADN 21	1200
Consensus	GCGGAGUAT	CGTGTATTA	TGTTATCAA	TGCGGATCG	TGACTGAGA	AGTTAAAGA	ATTGAGATC	GAATACAGG	TAGACGAGG	GAGCTTGGAA	ACACTGGACC	CTGGGGCTC	1320
Env ADN 6	1320
Env ADN 10	1320
Env ADN 21	1320

FIG. 2 suite



Consensus	CTCAGCCAAAT GGATGCCCTG GATTCGCCC TTCCTAGGAC CTCCTAGCAGC TATATATATG CTACTCTCT TTGGACCCCTG TATCTTTAAC CTCCTGTATA ACTTGTCTC TTCCAGATC	1440
ENV ADN 6	1440
ENV ADN 10	1440
ENV ADN 21	1440
Consensus	GAAGCTGTAA AACTACAAAT GGAGCCCAAG ATGCAGTCCA AGACTAAGAT CTACCGCAGA CCGCTGGACC GCGCTGCTAG CCCAGGATCT GATGTTAATG ACATCAAAGG CACCCCTCCT	1560
ENV ADN 6	1560
ENV ADN 10	1560
ENV ADN 21	1560
Consensus	GAGGAAATCT CAGCTGCACA ACCCTCTACTA CCGCCCAATT CAGCAGGAG CAGTTAG	1617
ENV ADN 6	1617
ENV ADN 10	1617
ENV ADN 21	1617



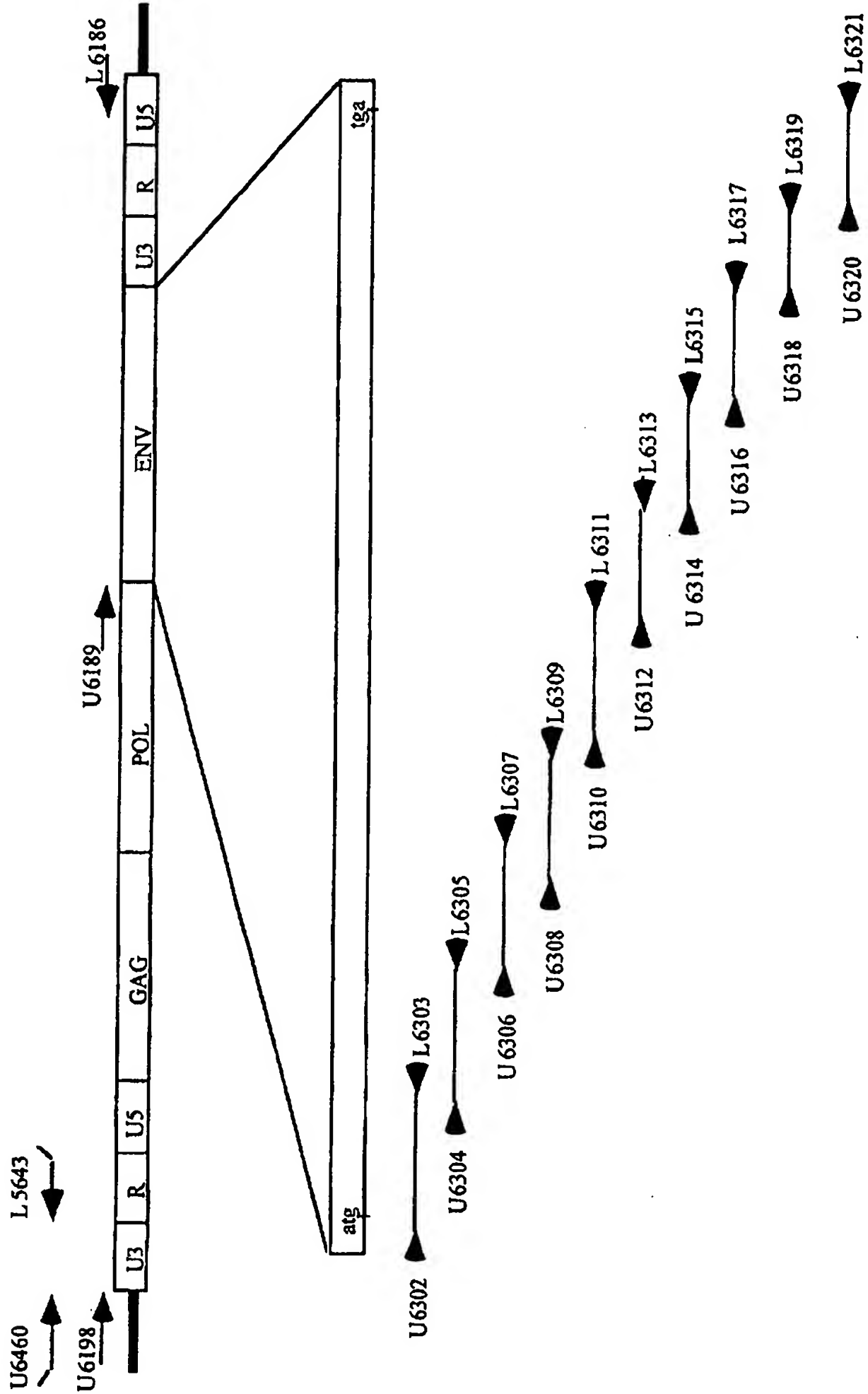
Consensus	TGACGACAG	GACTAGCTGG	ATTTCCTAGG	CGGACTAAGA	ATCCCTAAGC	CTAGCTGGGA	ARGTGACCAC	GTCGACCTTT	AAACAGGGGG	CTTGCARCTT	100
LTR6 c1A	100
LTR21 c1S	100
Consensus	AGCTCACACC	TGACCAATCA	GAGGCTTCAC	TAAATGCTA	ATTAGCCAAA	GACGCGAGGT	AAAGAAATAG	CCATCATCT	ATTGCTGAG	AGCACAGCAG	200
LTR6 c1A	200
LTR21 c1S	200
Consensus	GAGGACAAAY	RATGGGGATA	TAAACCCARG	YMTTCGAGCY	GGCAAC						246
LTR6 c1A						246
LTR21 c1S						246

FIG. 4



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FIGURE 4



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⑦③ Titulaire(s) :

⑦④ Mandataire(s) : GERMAIN ET MAUREAU.

⑤④ PROCÉDE DE DETECTION DE L'EXPRESSION D'UNE PROTEINE D'ENVELOPPE D'UN RETROVIRUS
ENDOGENE HUMAIN ET UTILISATIONS D'UN GENE CODANT POUR CETTE PROTEINE.

⑤⑦ Le procédé de détection de l'expression d'une protéine ou d'un polypeptide d'enveloppe d'un rétrovirus endogène humain, est caractérisé en ce que la protéine ou le polypeptide présente une séquence polypeptidique qui comprend la séquence SEQ ID NO: 1 ou un fragment de SEQ ID NO: 1 ou une séquence présentant, pour toute suite de 20 acides aminés, au moins 90% d'identité avec la séquence SEQ ID NO: 1 ou avec un fragment de SEQ ID NO: 1, et en ce qu'on détecte le pouvoir fusogène de ladite protéine ou dudit fragment dans des cellules d'un tissu cellulaire ou d'une culture cellulaire, par la mise en évidence de la formation de syncytia.

On utilise un gène ou un acide nucléique ou un fragment de ceux-ci pour préparer une composition thérapeutique ou prophylactique, notamment pour traiter des cancers et prévenir une déficience dans l'élaboration du placenta.

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